

A novel berry phenological scale based on gene expression

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Phenology scale systems widely adopted by viticulturists define stages of the annual development of the vine based on the visual description of well recognizable traits related to organ growth and morphology, including grape features from fruit set to maturity. However, although some stages can be easily described (e.g. fruit set, veraison), defining a comparable developmental stage for grapes of the same cultivar when grown in different conditions or for grapes of different cultivars can be challenging, in particular after the onset of ripening. By analysing transcriptomic data collected over berry development, it was shown that the variations of a portion of the transcriptome exhibited conserved dynamics across cultivars and growing condition of grapevines, and thus may be used to describe the developmental stage of berry development. In this work, we used the transcriptomic data generated from grape berries weekly sampled from Cabernet Sauvignon and Pinot noir vines grown in the same location over three consecutive vintages, focusing on conserved annual dynamics rather than on the biological significance of the expression program inferred by gene function. By interpolating the transcriptomic samples dispersed in a 3D space of a PCA we built a 30-stage Transcriptional Phenology Scale (TPhS) precisely defining the progression of development from berry formation to full ripening. The performance of the scale was assessed projecting onto the TPhS both RNA-seq and microarray transcriptomic samples from the same dataset used to elaborate the scale, and from several other public datasets. The results allowed to align samples on the new phenological scale and to highlight differences related to variables like the grape variety, the cultivation site, the vintage, or the applied treatment such as cluster thinning, defoliation, water limitation and temperature regimes. In some cases, the phenological re-scaling of sample collections from previous studies provided valuable hints to re-interpret the experimental results. Overall, we show that the transcriptomic information can be accessed to precisely define a transcriptional phenology scale that can be used to map the ontogenetic development of the fruit with high precision and to align the stage of berry development of different grapes.